Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

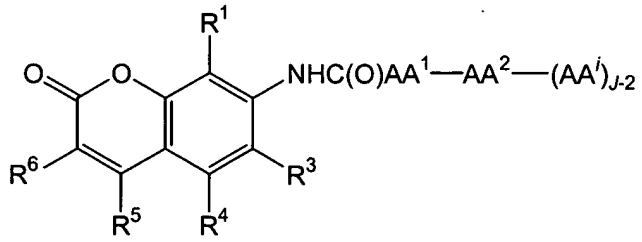
Listing of Claims:

1 (cancelled)

2 (currently amended) The material according to claim **5**, wherein said linking group R^{14} is a member selected from the group consisting of substituted or unsubstituted alkyl, substituted or unsubstituted heteroalkyl and substituted or unsubstituted aryl.

3-4 (cancelled)

5 (currently amended): A material having the structure:



wherein:

R^1, R^3, R^4, R^5 and R^6 are members independently selected from the group consisting of H, halogen, $-NO_2$, -CN, $-C(O)_mR^7$, $-C(O)NR^8R^9$, $-S(O)_tR^{10}$, $-SO_2NR^{11}R^{12}$, $-OR^{13}$, substituted or unsubstituted alkyl and $-R^{14}$-*SS*, with the proviso that at least one of R^1, R^3, R^4, R^5 and R^6 is $-R^{14}$-*SS*;

wherein:

R^7, R^8, R^9, R^{10}, R^{11}, R^{12} and R^{13} are members independently selected from the group consisting of H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl;

R^{14} is a linking group adjoining said fluorogenic moiety and said solid support;

m is a member selected from the group consisting of the integers 1 and 2;

t is a member selected from the group consisting of the integers from 0 to 2; and

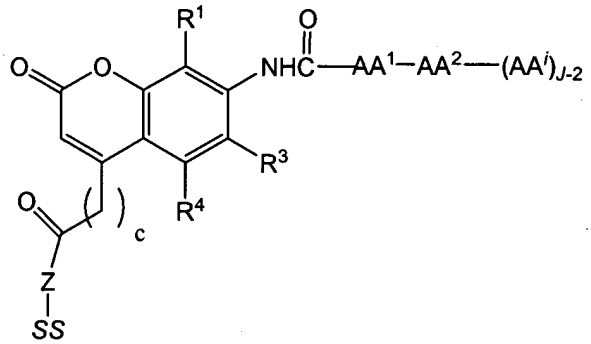
SS is a solid support;

AA^1-AA^2-$(AA^i)_{J-2}$ is a peptide sequence, wherein each of AA^1 through AA^i is an amino acid residue which is a member independently selected from the group of natural amino acid residues, unnatural amino acid residues and modified amino acid residues;

J denotes the number of amino acid residues forming said peptide sequence and is a member selected from the group consisting of the numbers from 2 to 10, such that *J*-2 is the number of amino acid residues in the peptide sequence exclusive of AA^1-AA^2; and

i denotes the position of said amino acid residue relevant to AA^1 and when *J* is greater than 2, *i* is a member selected from the group consisting of the numbers from 3 to 10.

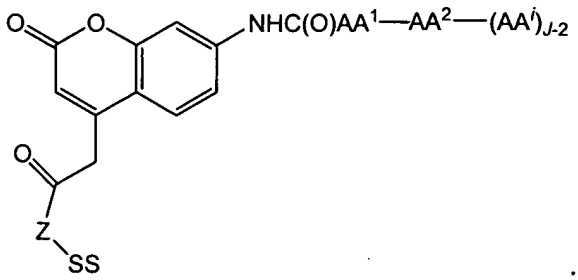
6 (currently amended): The material according to claim **5**, having the structure:



wherein: Z is a member selected from the group consisting of –O-, and –NR^{16}-, wherein R^{16} is H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl, and

c is a member selected from the integers from 0 to 6.

7 (currently amended): A material according to claim **6**, having the structure:



8 (currently amended): A method of assaying for the presence of an enzymatically active protease in a sample, said method comprising:

(a) contacting said sample with a material according to claim **5** in such a manner whereby said fluorogenic moiety is released from said peptide sequence upon action of said protease, thereby producing a fluorescent moiety; and

(b) observing whether said sample undergoes a detectable change in fluorescence, said detectable change being an indication of the presence of said enzymatically active protease in said sample.

9 (original): The method according to claim **8**, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, metalloprotease and serine protease.

10 (original): The method according to claim **8**, wherein said protease is a protease of a microorganism.

11 (original): The method according to claim **10**, wherein said microorganism is a member selected from the group consisting of bacteria, fungi, yeast, viruses, and protozoa.

12 (original): The method according to claim **8**, wherein said sample is a clinical sample from a subject.

13 (original): The method according to claim **8,** further comprising (c) quantifying said fluorescent moiety, thereby quantifying said protease.

14 (currently amended): A method of assaying for the presence of a selected microorganism in a sample by probing the sequence specificity of peptide cleavage by a protease of said microorganism, said method comprising:

(a) contacting a sample suspected of containing said selected microorganism with a material according to claim **5**, wherein said peptide comprises a sequence that is selectively cleaved by said protease of said selected microorganism, thereby releasing the fluorogenic moiety from the peptide sequence;

(b) detecting the cleavage by detecting fluorescence arising from a fluorescent moiety produced by cleavage of said fluorogenic moiety from said peptide sequence, thereby confirming said presence of said selected microorganism in said sample.

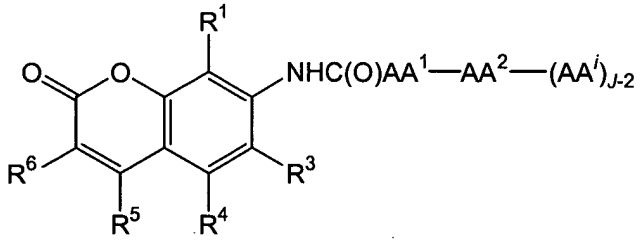
15 (original): The method according to claim **14**, further comprising (c) quantifying said fluorescence, thereby quantifying said protease of said microorganism.

16 (cancelled)

17 (currently amended): The fluorogenic peptide according to claim **18**, wherein Y is an organic functional group selected from the group consisting of $-COOR^{17}$, $CONR^{17}R^{21}$, $-C(O)R^{17}R^{21}$, $-OR^{17}$, $-SR^{17}$, $-C(O)SR^{17}$ and $-NR^{17}R^{21}$

wherein, R^{17} and R^{21} are members independently selected from H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl.

18 (currently amended): A fluorogenic peptide having the structure:



wherein:

R^1, R^3, R^4, R^5 and R^6 are members independently selected from the group consisting of H, halogen, $-NO_2$, -CN, $-C(O)_mR^{6'}$, $-C(O)NR^7R^8$, $-S(O)_tR^9$, $-SO_2NR^{10}R^{11}$, $-OR^{12}$, substituted or unsubstituted alkyl, -NHC(O)-P, and $-R^{20}$-Y, with the proviso that at least one of R^1, R^3, R^4, R^5 and R^6 is $-R^{20}$-Y,

wherein:

$R^{6'}$, R^7, R^8, R^9, R^{10}, R^{11} and R^{12} are members independently selected from the group consisting of H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl;

R^{20} is either present or absent and is a member selected from the group consisting of substituted or unsubstituted alkyl and substituted or unsubstituted heteroalkyl;

Y is a member selected from the group consisting of organic functional groups and methyl;

m is a member selected from the group consisting of the integers 1 and 2; and

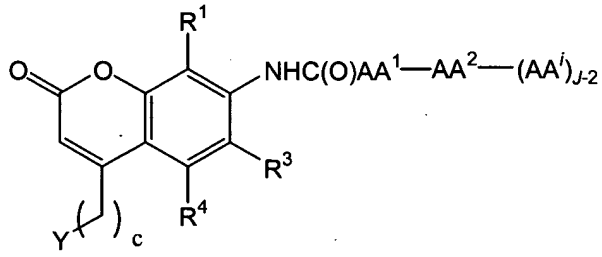
t is a member selected from the group consisting of the integers from 0 to 2.

AA^1-AA^2-$(AA^i)_{J-2}$ is a peptide sequence, wherein each of AA^1 through AA^i is an amino acid residue which is a member independently selected from the group of natural amino acid residues, unnatural amino acid residues and modified amino acid residues;

J denotes the number of amino acid residues forming said peptide sequence and is a member selected from the group consisting of the numbers from 2 to 10, such that *J*-2 is the number of amino acid residues in the peptide sequence exclusive of AA^1-AA^2; and

i denotes the position of said amino acid residue in sequence relative to AA^1 and when *J* is greater than 2, *i* is a member selected from the group consisting of the numbers from 3 to 10.

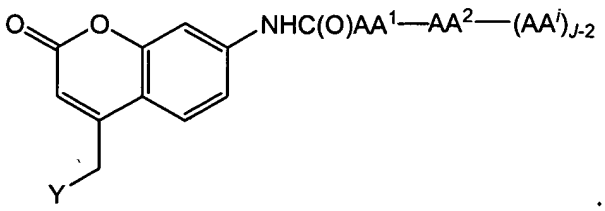
19 (original): A fluorogenic peptide according to claim **18**, having the structure:



wherein:

c is a member selected from the group consisting of the integers from 0 to 6.

20 (original): A fluorogenic peptide according to claim **19**, having the structure:



21 (original): The fluorogenic peptide according to claim **18**, wherein said peptide sequence comprises a peptide bond that is cleaved by a protease releasing said fluorogenic moiety from said peptide sequence, thereby producing a fluorescent moiety and a peptide moiety.

22 (original): The fluorogenic peptide according to claim **21**, wherein said peptide bond is formed between a carboxyl of the carboxy-terminus amino acid residue and an amine group of said fluorogenic moiety.

23 (currently amended): A method of assaying for the presence of an enzymatically active protease in a sample, said method comprising:

(a) contacting a sample suspected of containing said protease with a peptide according to claim **18** in such a manner whereby said fluorogenic moiety is released from said peptide sequence upon action of said protease, thereby producing a fluorescent moiety; and

(b) observing whether said sample undergoes a detectable change in fluorescence, said detectable change being an indication of the presence of said enzymatically active protease in said sample.

24 (original): The method according to claim **23**, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, metalloprotease and serine protease.

25 (original): The method according to claim **23**, wherein said protease is a protease of a microorganism.

26 (original): The method according to claim **25**, wherein said microorganism is a member selected from the group consisting of bacteria, fungi, yeast, viruses, and protozoa.

27 (original): The method according to claim **23**, wherein said sample is a clinical sample from a subject.

28 (original): The method according to claim **27**, wherein said subject is a human.

29 (original): The method according to claim **23**, further comprising (c) quantifying said fluorescent moiety, thereby quantifying said protease.

30 (currently amended): A method of assaying for the presence of a selected microorganism in a sample by probing the sequence specificity of peptide cleavage by a protease of said microorganism, said method comprising:

(a) contacting a sample suspected of containing said selected microorganism with a material according to claim **18**, wherein said peptide comprises a sequence that is selectively cleaved by a protease of a selected microorganism, thereby releasing said fluorogenic moiety from said peptide sequence;

(b) detecting said cleavage by detecting fluorescence arising from a fluorescent moiety produced by cleavage of said fluorogenic moiety from said peptide sequence, thereby confirming said presence of said selected microorganism in said sample.

31 (original): The method according to claim **30**, further comprising (c) quantifying said fluorescence, thereby quantifying said protease of said microorganism.

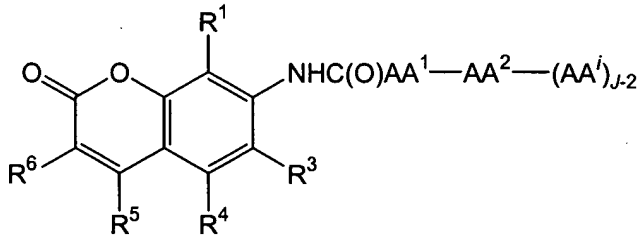
32 (cancelled)

33 (currently amended): The library according to claim **35**, wherein said linking group R^{14} is a member selected from the group consisting of substituted or unsubstituted alkyl, substituted or unsubstituted heteroalkyl and substituted or unsubstituted aryl.

34 (currently amended): The library according to claim **35**, wherein Y is an organic functional group selected from the group consisting of $-COOR^{17}$, $CONR^{17}R^{21}$, $-C(O)R^{17}R^{21}$, $-OR^{17}$, $-SR^{17}$, $-C(O)SR^{17}$, and $-NR^{17}R^{21}$

wherein, R^{17} and R^{21} are members independently selected from H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl.

35 (currently amended): A library of fluorogenic peptides comprising at least a first peptide having a first peptide sequence covalently attached to a first fluorogenic moiety and a second peptide having a second peptide sequence covalently attached to a second fluorogenic moiety, said first peptide and said second peptide having the structure:



wherein:

R^1, R^3, R^4, R^5, and R^6 are members independently selected from the group consisting of H, halogen, $-NO_2$, -CN, $-C(O)_mR^7$, $-C(O)NR^8R^9$, $-S(O)_tR^{10}$, $-SO_2NR^{11}R^{12}$, $-OR^{13}$, substituted or unsubstituted alkyl, -NH-C(O)-P, R^{20}-Y and $-R^{14}$-*SS*, with the proviso that for each peptide at least one of R^1, R^3, R^4, R^5 and R^6 is a member independently selected from $-R^{14}$-*SS* and R^{20}-Y,

wherein:

R^7, R^8, R^9, R^{10}, R^{11}, R^{12} and R^{13} are members independently selected from the group consisting of H, substituted or unsubstituted alkyl and substituted or unsubstituted aryl;

R^{14} is a linking group adjoining said fluorogenic moiety and the solid support;

R^{20} is either present or absent and is a member selected from the group consisting of substituted or unsubstituted alkyl and substituted or unsubstituted heteroalkyl;

Y is a member selected from the group consisting of organic functional groups and methyl;

m is a member selected from the group consisting of the integers from 1 to 2;

t is a member selected from the group consisting of the integers from 0 to 2; and

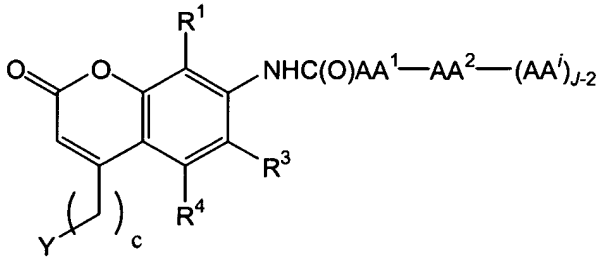
SS is a solid support;

AA^1-AA^2-$(AA^i)_{J-2}$ is a peptide sequence, wherein each of AA^1 through AA^i is an amino acid residue which is a member independently selected from the group of natural amino acid residues, unnatural amino acid residues and modified amino acid residues;

J denotes the number of amino acid residues forming said peptide sequence and is a member selected from the group consisting of the numbers from 2 to 10, such that *J*-2 is the number of amino acid residues in the peptide sequence exclusive of AA^1-AA^2; and

i denotes the position of said amino acid residue in sequence relative to AA^1 and when *J* is greater than 2, *i* is a member selected from the group consisting of the numbers from 3 to 10.

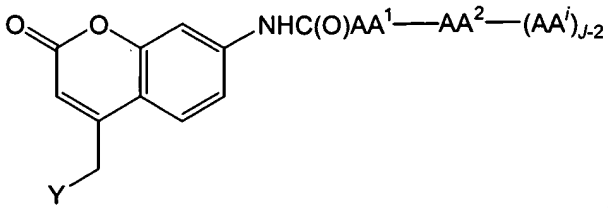
36 (currently amended): The library of fluorogenic peptides according to claim **35**, wherein said first peptide and said second peptide have the structure:



wherein:

c is a member selected from the group consisting of the numbers from 0 to 6.

37 (original): The library of fluorogenic peptides according to claim **36**, wherein said first peptide and said second peptide have the structure:



38 (currently amended): The library according to claim **35**, wherein said fluorogenic moiety of said first peptide and said fluorogenic moiety of said second peptide are different fluorogenic moieties.

39 (currently amended): The library according to claim **35**, wherein said first peptide sequence and said second peptide sequence are identical.

40 (currently amended): The library according to claim **35**, wherein said first peptide sequence and said second peptide sequence are different.

41 (currently amended): The library according to claim **40**, wherein an amino acid residue selected from the group consisting of AA^1, AA^2, AA^i and combinations thereof of said first peptide is a different amino acid residue than an amino acid residue at a corresponding position relative to AA^1 of said second peptide.

42 (currently amended): The library according to claim **35**, wherein AA^1 of said first peptide sequence and AA^1 of said second peptide sequence are identical amino acid residues.

43 (currently amended): The library according to claim **35**, wherein AA^1 of said first peptide sequence and AA^1 of said second peptide sequence are different amino acid residues.

44 (currently amended): The library according to claim **35**, wherein AA^2 of said first peptide sequence and AA^2 of said second peptide sequence are identical amino acid residues.

45 (currently amended): The library according to claim **35**, wherein AA^2 of said first peptide sequence and AA^2 of said second peptide sequence are different amino acid residues.

46 (currently amended): The library according to claim **35**, wherein AA^i of said first peptide sequence and AA^i of said second peptide sequence are identical amino acid residues.

47 (currently amended): The library according to claim **35,** wherein AA^i of said first peptide sequence and AA^i of said second peptide sequence are different amino acid residues.

48 (original): The library according to claim **42**, comprising at least six peptides having different peptide sequences, wherein AA^1 is a different amino acid residue in each of said different peptide sequences.

49 (original): The library according to claim **48**, comprising at least twelve peptides having different peptide sequences wherein AA^1 is a different amino acid residue in each of said different peptide sequences.

50 (original): The library according to claim **49**, comprising at least twenty peptides having different peptide sequences wherein AA^1 is a different amino acid residue in each of said different peptide sequences.

51 (currently amended): The library according to claim **35**, wherein AA^1 is a member selected from the group consisting of Lys, Arg, Leu and combinations thereof.

52 (currently amended): The library according to claim **35**, wherein *J* is a member selected from the numbers from 4 to 8.

53 (currently amended): The library of peptides according to claim **35**, wherein at least one of said first peptide and said second peptide is cleavable by a protease into a fluorescent moiety and the peptide sequence.

54 (currently amended): The library according to claim **35**, comprising at least 10 peptides, wherein each of the peptide sequences is a different peptide sequence.

55 (original): The library according to claim **54**, comprising at least 100 peptides, wherein each of the peptide sequences is a different peptide sequence.

56 (original): The library according to claim **55**, comprising at least 1,000 peptides, wherein each of the peptide sequences is a different peptide sequence.

57 (original): The library according to claim **56**, comprising at least 10,000 peptides, wherein each of the peptide sequences is a different peptide sequence.

58 (original): The library according to claim **57**, comprising at least 100,000 peptides, wherein each of the peptide sequences is a different peptide sequence.

59 (original): The library according to claim **58** comprising at least 1,000,000 peptides, wherein each of the peptide sequences is a different peptide sequence.

60 (currently amended): The library according to claim **35**, wherein said first peptide is located at a first region of a substrate and said second peptide is located at a second region of a substrate.

61 (currently amended): A method of determining a peptide sequence specificity profile of an enzymatically active protease, said method comprising:

(a) contacting said protease with a library of peptides according to claim **35** in such a manner whereby the fluorogenic moiety is released from the peptide sequence, thereby forming a fluorescent moiety;

(b) detecting said fluorescent moiety;

(c) determining the sequence of said peptide sequence, thereby determining said peptide sequence specificity profile of said protease.

62 (original): The method according to claim **61**, further comprising (d) quantifying said fluorescent moiety, thereby quantifying said protease.

63 (original): A database comprising at least one set of peptide sequence specificity data for a protease determined using a library according to claim **35**.

64 (original): The database according to claim **63**, wherein said database is an electronic database.

65 (original): The database according to claim **64**, wherein said database is distributed on a wide area network.

66 (original): A database comprising at least one set of peptide sequence specificity data for a protease determined using a method according to claim **61**.

67 (original): The database according to claim **63**, wherein said database is an electronic database.

68 (original): The database according to claim **64**, wherein said database is distributed on a wide area network.

69 (currently amended): The method according to claim **61**, wherein said protease is a member selected from the group consisting of aspartic protease, cysteine protease, and serine protease.

70 (original): The method according to claim **61**, wherein said protease is a protease of a microorganism.

71 (original): The method according to claim **70**, wherein said microorganism is a member selected from the group consisting of bacteria, fungi, yeast, viruses, and protozoa.

72 (original): The method according to claim **61**, further comprising (c) quantifying the fluorescent moiety, thereby quantifying said protease.

73-83 (cancelled)